Claim 1 (amended):

An isolated peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *msl* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 2 (amended):

The isolated peptide, according to claim 1, comprising an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

Claim 3 (amended):

An isolated polynucleotide which comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *msl* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 4 (amended):

A host transformed to express a peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *msl* to *ms16*, obtainable from *E. coli* K1, or a

homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 5 (amended):

A vaccine comprising a peptide, or the means for its expression, wherein said peptide is encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 6 (amended):

A vaccine comprising a microorganism having a virulence gene mutation, wherein the gene is selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 7 (amended):

The vaccine, according to claim 6, wherein said virulence gene mutation comprises a virulence gene deletion in two genes, wherein one gene encodes *tatA* and the other encodes *tatE*.

Claim 8 (amended):

The vaccine, according to claim 6, wherein the gene lies within a pathogenicity island.

Claim 9 (amended):

A method for screening potential drugs, or for the detection of virulence, wherein said method utilizes a peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA, tatB, tatC, tatE, mdoG, creC, recG, yggN, eck1, iroD, iroC, iroE, mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 10 (amended):

A method for treatment or prevention of a condition associated with infection by a Gram-negative bacterium, said method comprising administering a vaccine to a person or animal in need thereof, wherein said vaccine comprises a peptide, or a host transformed to express said peptide, wherein said peptide is encoded by an operon comprising a gene selected from the group consisting of *tatA, tatB, tatC, tatE, mdoG, creC, recG, yggN, eck1, iroD, iroC, iroE, mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 11 (amended):

The method, according to ~~claim~~ 10, wherein the bacterium is *E. coli*.

Please add the following new claims:

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12. The polynucleotide, according to claim 3, wherein said gene encodes a peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

13. The host, according to claim 4, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

14. The vaccine, according to claim 5, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

15. The vaccine, according to claim 6, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

16. The vaccine, according to claim 15, wherein said virulence gene mutation comprises a virulence gene deletion in two genes, wherein one gene encodes *tatA* and the other encodes *tatE*.

17. The vaccine, according to claim 15, wherein the gene lies within a pathogenicity island.

18. The method, according to claim 9, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

19. The method, according to claim 9, wherein said peptide comprises an amino acid sequence as set forth in SEQ ID NO. 33.

20. The method, according to claim 10, wherein said peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 5, 7, 9, 11, 12, 13, 14, 16, 18, 19, 21, 23, 24, 25, 26, 28, 29, 31, 32 and 35-48.

21. The method, according to claim 20, wherein the bacterium is *E. coli.*

22. A method for treatment or prevention of a condition associated with infection by a Gram-negative bacterium, said method comprising administering a nucleotide to a person or animal in need thereof, wherein said nucleotide comprises an operon including a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eck1*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.